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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/246,129ADATE: 11/16/1999
TIME: 15:00:10

Input Set: I246129A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Yu, Guo-Liang
2 Ni, Jian
3 Rosen, Craig A.
4 <120> TITLE OF INVENTION: Tumor Necrosis Factor Gamma
5 <130> FILE REFERENCE: PF141P4
6 <140> CURRENT APPLICATION NUMBER: US/09/246,129A
7 <141> CURRENT FILING DATE: 1999-02-08
8 <150> EARLIER APPLICATION NUMBER: 60/074,047
9 <151> EARLIER FILING DATE: 1998-02-09
10 <150> EARLIER APPLICATION NUMBER: 09/131,237
11 <151> EARLIER FILING DATE: 1998-08-07
12 <150> EARLIER APPLICATION NUMBER: 09/005,020
13 <151> EARLIER FILING DATE: 1998-01-09
14 <150> EARLIER APPLICATION NUMBER: 08/461,246
15 <151> EARLIER FILING DATE: 1995-06-05
16 <150> EARLIER APPLICATION NUMBER: PCT/US94/12880
17 <151> EARLIER FILING DATE: 1994-11-07
18 <160> NUMBER OF SEQ ID NOS: 24
19 <170> SOFTWARE: PatentIn Ver. 2.0
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21 <211> LENGTH: 2442
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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26 <222> LOCATION: (783)..(1304)
27 <220> FEATURE:
28 <221> NAME/KEY: mat_peptide
29 <222> LOCATION: (864)..(1304)
30 <220> FEATURE:
31 <221> NAME/KEY: sig_peptide
32 <222> LOCATION: (783)..(863)
33 <220> FEATURE:
34 <221> NAME/KEY: misc_feature /
35 <222> LOCATION: (2265)
36 <223> OTHER INFORMATION: n equals a, t, g, or c
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39 <222> LOCATION: (2273)
40 <223> OTHER INFORMATION: n equals a, t, g, or c
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42 <221> NAME/KEY: misc_feature /
43 <222> LOCATION: (2307)
44 <223> OTHER INFORMATION: n equals a, t, g, or c

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55 <222> LOCATION: (2379)
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60      gacagtgcag aaggatatgt tagaaccac tgaaaacct gaaggttgaa aaggaagcat 180
61      accctcctga cctataagaa aattttcagt ctgcaggggg atatccttgt ggcccaagac 240
62      attggtgta tcatttgact aagaggaaat tatttgtggt gagctctgag tgaggattag 300
63      gaccaggag atgccaagtt tctatcactt acctcatgcc tgtaagacaa gtgttttgtt 360
64      ccaattgatg aatggggaga aaacagttca gccaatcact tatgggcaca gaatggaatt 420
65      tgaagggctt ggtgcctgcc cttgtcatac gtaaacaaga gaggcacga tgagttttat 480
66      ctgagtcatt tgggaaagga taattcttgc accaagccat tttcctaaac acagaagaat 540
67      agggggattc cttaaccttc attgttctcc aggatcatag gtctcaggat aaattaaaaa 600
68      ttttcaggtc agaccactca gtctcagaaa ggcaaagtaa tttgcccag gtcactagtc 660
69      caagatgtta ttctctttga acaaatgtgt atgtccagtc acatattctt cattcattcc 720
70      tccccaaagc agtttttagc tgtaggtat attcgatcac tttagtctat tttgaaaatg 780
71      at atg aga cgc ttt tta agc aaa gtc tac agt ttc cca atg aga aaa 827
72      Met Arg Arg Phe Leu Ser Lys Val Tyr Ser Phe Pro Met Arg Lys
73      -25 -20 -15
74      tta atc ctc ttt ctt gtc ttt cca gtt gtg aga caa act ccc aca cag 875
75      Leu Ile Leu Phe Leu Val Phe Pro Val Val Arg Gln Thr Pro Thr Gln
76      -10 -5 -1 1
77      cac ttt aaa aat cag ttc cca gct ctg cac tgg gaa cat gaa cta ggc 923
78      His Phe Lys Asn Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly
79      5 10 15 20
80      ctg gcc ttc acc aag aac cga atg aac tat acc aac aaa ttc ctg ctg 971
81      Leu Ala Phe Thr Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu
82      25 30 35
83      atc cca gag tcg gga gac tac ttc att tac tcc cag gtc aca ttc cgt 1019
84      Ile Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg
85      40 45 50
86      ggg atg acc tct gag tgc agt gaa atc aga caa gca ggc cga cca aac 1067
87      Gly Met Thr Ser Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn
88      55 60 65
89      aag cca gac tcc atc act gtg gtc atc acc aag gta aca gac agc tac 1115
90      Lys Pro Asp Ser Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr
91      70 75 80
92      cct gag cca acc cag ctc ctc atg ggg acc aag tct gta tgc gaa gta 1163
93      Pro Glu Pro Thr Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val
94      85 90 95 100

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96 Gly Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu
97 105 110 115
98 caa gaa ggg gac aag cta atg gtg aac gtc agt gac atc tct ttg gtg 1259
99 Gln Glu Gly Asp Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val
100 120 125 130
101 gat tac aca aaa gaa gat aaa acc ttc ttt gga gcc ttc tta cta 1304
102 Asp Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
103 135 140 145
104 taggaggaga gcaaatatca ttatatgaaa gtcctctgcc accgagttcc taatttttctt 1364
105 tgttcaaagt taattataac caggggtttt cttggggccg ggagtagggg gcattccaca 1424
106 gggacaacgg tttagctatg aaatttgggg ccaaaatttc acacttcatg tgccttactg 1484
107 atgagagtac taactggaaa aaggctgaag agagcaaata tattattaag atgggttgga 1544
108 ggattggcga gtttctaaat attaaagacac tgatcactaa atgaatggat gatctactcg 1604
109 ggtcaggatt gaaagagaaa tatttcaaca cctccctgct atacaatggg caccagtggg 1664
110 ccagttattg ttcaatttga tcataaattt gcttcaattc aggagctttg aaggaagtcc 1724
111 aaggaaagct ctagaaaaca gtataaactt tcagaggcaa aatccttcac caatttttcc 1784
112 acatactttc atgccttgcc taaaaaaaat gaaaagagag ttggtatgtc tcatgaatgt 1844
113 tcacacagaa ggagttgggt ttcattgtcat ctacagcata tgagaaaagc taccttttctt 1904
114 ttgattatgt acacagatat cttaaataagg aagtttgagt ttcacatgta tatcccaa 1964
115 acaacagttg cttgtattca gtagagtttt cttgccacc tattttgtgc tgggttctac 2024
116 cttaaccag aagacactat gaaaaacaag acagactcca ctcaaattt atatgaacac 2084
117 cactagatac ttctgatca aacatcagtc aacatactct aaagaataac tccaagtctt 2144
118 ggccaggcgc agtggctcac acctgtaate ccaacacttt gggaggccaa ggtgggtgga 2204
119 tcatctaagg ccgggagttc aagaccagcc tgaccaacgt ggagaaaccc catctctact 2264
120 naaaatacna aattagccgg gcgtggtagc gcatggctgt aancctggct actcaggagg 2324
121 ccgaggcaga anaatttctt gaactgggga ggcagaggtt gcggtgagcc cagancgcgc 2384
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125 <212> TYPE: PRT
126 <213> ORGANISM: Homo sapiens
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131 -10 -5 -1 1 5
132 Phe Lys Asn Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu
133 10 15 20
134 Ala Phe Thr Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu Ile
135 25 30 35
136 Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly
137 40 45 50
138 Met Thr Ser Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys
139 55 60 65
140 Pro Asp Ser Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro
141 70 75 80 85
142 Glu Pro Thr Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly
143 90 95 100
144 Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln

W-OK
W-5

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147          120          125          130
148      Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
149          135          140          145
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158          20          25          30
159      Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
160          35          40          45
161      Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
162          50          55          60
163      Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
164          65          70          75          80
165      Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
166          85          90          95
167      Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
168          100          105          110
169      Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
170          115          120          125
171      Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
172          130          135          140
173      Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
174          145          150          155          160
175      Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
176          165          170          175
177      Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
178          180          185          190
179      Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
180          195          200          205
181      Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
182          210          215          220
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184          225          230
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188 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 4
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192      Leu His Leu Leu Leu Leu Gly Leu Leu Val Leu Leu Pro Gly Ala
193          20          25          30
194      Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala

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195          35          40          45
196 Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
197          50          55          60
198 Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
199          65          70          75          80
200 Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
201          85          90          95
202 Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
203          100          105          110
204 Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Thr Ser Ser Pro
205          115          120          125
206 Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe
207          130          135          140
208 His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
209          145          150          155          160
210 Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
211          165          170          175
212 Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
213          180          185          190
214 Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
215          195          200          205
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217 <211> LENGTH: 244
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens
220 <400> SEQUENCE: 5
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224          20          25          30
225 Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
226          35          40          45
227 Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln
228          50          55          60
229 Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu
230          65          70          75          80
231 Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro
232          85          90          95
233 Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe
234          100          105          110
235 Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro
236          115          120          125
237 Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg
238          130          135          140
239 Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg
240          145          150          155          160
241 Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu
242          165          170          175
243 Leu Leu Leu Glu Gly Ala Glu Thr Val Pro Val Leu Asp Pro Ala
244          180          185          190

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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355	W	"N" or "Xaa" used: Feature required	caagaagggg acnagctaag ggtgaacgct agtgacat
359	W	"N" or "Xaa" used: Feature required	ggggggccca aaatttcaca acttcatngt tgccttta
360	W	"N" or "Xaa" used: Feature required	gganaaaagg cttg
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443	W	"N" or "Xaa" used: Feature required	ggaccaggng gtgnccaagt ttctatcact tacctcat
444	W	"N" or "Xaa" used: Feature required	tcccattgnt gatgggggta aaacnttcag ccatacact
445	W	"N" or "Xaa" used: Feature required	ganggggttg ngcnggnctt gtcntcgtaa acaggggg
446	W	"N" or "Xaa" used: Feature required	ttgggnagga ctt
480	W	"N" or "Xaa" used: Feature required	ggcagagggt caatttgatc ataaatttgc ttcaattc
484	W	"N" or "Xaa" used: Feature required	tgattatgta cacaggnttc taaataagga agtatgag
485	W	"N" or "Xaa" used: Feature required	acaacagttg cttgtnttca gttnggggtt ttcttggc
486	W	"N" or "Xaa" used: Feature required	gttctanctt taaccccnag
532	W	"N" or "Xaa" used: Feature required	ggcacagcng gnagtagggg gcattccaca gggacaac
533	W	"N" or "Xaa" used: Feature required	cccaaaattt cacacttcat gtgccttact gatgagag
537	W	"N" or "Xaa" used: Feature required	atnaatttgc nttcaattcc aggagctttg gaaggaat
538	W	"N" or "Xaa" used: Feature required	ccgtattaaa ctttccaggg gccaaantcc ttcaccaa
539	W	"N" or "Xaa" used: Feature required	cctgncncaa aaaaatggaa agggagtgtg tangtccc
601	W	"N" or "Xaa" used: Feature required	ctgcactggg nncatgaact aggcctggcc ttcaccaa
602	W	"N" or "Xaa" used: Feature required	aaattcctgc tgatcccaga ntcgggagac tacttcat
603	W	"N" or "Xaa" used: Feature required	gggaatgaac ctctgaantg ccagtgaaaa tcagncaa
604	W	"N" or "Xaa" used: Feature required	antccatnca ctgtggtcat caccaaggta acagacag
605	W	"N" or "Xaa" used: Feature required	cttcatgggg accaagtttg tttgcgaant aggttagc
606	W	"N" or "Xaa" used: Feature required	cttggggggc agttctnctt gncaagaagg ggacaagc
607	W	"N" or "Xaa" used: Feature required	tcnttttttg gtggnntttac acaaaagg
742	W	"N" or "Xaa" used: Feature required	tctacacaag gtacngacng ctaccctgag ccaaccca
744	W	"N" or "Xaa" used: Feature required	caagaagggg acnagctaag ggtgaacgct agtgacat
748	W	"N" or "Xaa" used: Feature required	ggggggccca aaatttcaca acttcatngt tgccttta
749	W	"N" or "Xaa" used: Feature required	gganaaaagg cttg
859	W	"N" or "Xaa" used: Feature required	attncggnac gagcagnggc atgnccgngg nnctnnga
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862	W	"N" or "Xaa" used: Feature required	tgcttgtcag ccagcttcgg gnccaggngg aggcctgt
863	W	"N" or "Xaa" used: Feature required	gacaggagtt tgcaccttca catcagcaag tttatgca
864	W	"N" or "Xaa" used: Feature required	agccangggg acaactgaca nttgtgagac aaattcca
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927	W	"N" or "Xaa" used: Feature required	ctgcactggg nncatgaact aggcctggcc ttcaccaa
928	W	"N" or "Xaa" used: Feature required	aaattcctgc tgatcccaga ntcgggagac tacttcat
929	W	"N" or "Xaa" used: Feature required	gggaatgaac ctctgaantg ccagtgaaaa tcagncaa
930	W	"N" or "Xaa" used: Feature required	antccatnca ctgtggtcat caccaaggta acagacag
931	W	"N" or "Xaa" used: Feature required	cttcatgggg accaagtttg tttgcgaant aggttagc
932	W	"N" or "Xaa" used: Feature required	cttggggggc agttctnctt gncaagaagg ggacaagc
933	W	"N" or "Xaa" used: Feature required	tcnttttttg gtggnntttac acaaaagg
979	W	"N" or "Xaa" used: Feature required	ggcacagcng gnagtagggg gcattccaca gggacaac
980	W	"N" or "Xaa" used: Feature required	cccaaaattt cacacttcat gtgccttact gatgagag
984	W	"N" or "Xaa" used: Feature required	atnaatttgc nttcaattcc aggagctttg gaaggaat
985	W	"N" or "Xaa" used: Feature required	ccgtattaaa ctttccaggg gccaaantcc ttcaccaa
986	W	"N" or "Xaa" used: Feature required	cctgncncaa aaaaatggaa agggagtgtg tangtccc